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SEQ ID NO: 6 A33 1 M V G K M W P V L W T L C A V R V T V D A I S V E T P Q D V L R A S Q G K S V T L P C T Y H T S T S
SEQ ID NO: 1 40628 1 M G T K A Q V E R K L L C L F I L A I L L C S L A L G S V T V H S S E P E V R I P E
SEQ ID NO: 2 45416 1 M G I L L G L L L G H L T V D T Y G R P I L E V P E S V T G P W K G D V N L P C T Y O P L
SEQ ID NO: 9 35638 1 M A R R S R H R L L L L L R Y L V V A L G Y H K A Y G F S A P K D Q Q V T A V E
SEQ ID NO: 10 JAM 1 . M G T E G K A G R K L L F L F T S M I L G S L V Q G K G S V Y T A Q S D V Q V P E

A33 51 S R E G L I Q W D K L L L T H T E R V V I W P F S N K N Y I H G E L Y K N R V S I S N H A E Q S D A
40628 43 N N P V K L S C A Y S G F S S P R V E W K F D Q G D T T R L V C Y N N K I T A S Y E D R V T F L P T
45416 47 Q G Y T Q V L V K W L V Q R G S D P V T I F L R D S S G D H I Q Q A K Y Q G R L H V S H K V P G D V
35638 43 Y Q E A I L A C K T P K X T V S S R L E W K K L G R S V S F V Y Q Q T L Q G D F K N R A E M I D F
JAM 42 N E S I K L T C T Y S G F S S P R V E W K F V Q G S T T A L V C Y N S Q I T A P Y A D R V T F S S S

A33 101 S I T I D Q L T M A D N G T Y E C S V S L . M S D L E G N T K S R V R L L V L V P P S K
40628 93 G I T F K S V T R E D T G T Y T C M V S E E G G N S Y G E V K V K L I V L V P P S K
45416 97 S L Q L S T L E M D D R S H Y T C E V T W O T P D G N Q V V R D K I T E L R V Q K L S V S K P T V T
35638 93 N I R I K N V T R S D A G K Y R C E V S A P S E Q Q N L E E D T V T L E V L V A P A V
JAM 92 G I T F S S V T R K D N G E Y T C M V S E E G G Q N Y G E V S I H L T T V L V P P S K

A33 144 P E C G I E G E T I I G N N I O L T C Q S K E G S P T P Q Y S W K R Y N I L N Q E Q
40628 135 P T V N I P S S A T I G N R A V L T C S E Q D G S P P S E Y T W F K D G I V M P T N . P K S T R A F
45416 147 T G S G Y G F T V P Q G M R I S L Q C Q A R . G S P P I S Y I W Y K Q O T N N Q E P
35638 137 P S C E V P S S A L S G T V V E L R C Q D K E G N P A P E Y T W F K D G I R L L E N . P R L G S Q S
JAM 134 P T I S V P S S V T I G N R A V L T C S E H D G S P P S E Y S W F K D G I S M L T A D A K K T R A F

FIG.-1A

SEQ ID NO: 6 A33 186 ... PLAQPASGQPVS LKNI STDTSGYI CTSSNEEG... TQFCNITY
 SEQ ID NO: 1 40628 184 SNSSYYLHP TTTGELVFDP LSA S DTGEYSCEARNGYG... TPMTSNAY
 SEQ ID NO: 2 45416 188 ... IKVATLSTLLFKP AVIA DSGSYFCTAKGQV GSEQHSDIYKFVVKD
 SEQ ID NO: 9 35638 186 TNSSYTMNTKT GTLQFN TVSKL DTGEYSCEARN SVG... YRRCPGKR
 SEQ ID NO: 10 JAM 184 MNSSFTIDPKSGD LIFDPVTAFDSGEY YCOAQN GYG... TAMRSEAA

A33 227 AYRSPSMNV ALYVGI AVGVVAA LIIIGII YCCCCRGKDDNT EDKEDA...
 40628 228 RMEAVERNVGV IVAAYLVTL LIL LGILVFGI WFAYSRGHFDRT KKGTS...
 45416 233 SSKLLKTKTEAPT TMTYPLKATSTYKQSWD WTTDM DGYLGETSAGPGKSL
 35638 230 WQVDDL NISGII AA VVVALVISVCGL GVCYAQRKGYFSKETSFKS...
 JAM 228 HMDAVELNVGG IVAAYLVTL LIL LGLLIFGV WFAYSRGYFETTKKGTAP...

A33 275 RPNREAYEPPPEQLREL SREREEEDDYRQEEQRSTGRES PDHLDQ
 40628 275 ... SKKV IYSQPSARSEGEFKQTSSFLV...
 45416 283 PVFAIIL IISLCCMVVFTMAYIMLCRKTSQ QEHVVEAAR...
 35638 277 NSSSKATTM SENVQWLT PVIPALWKAAAGGSRGQEF...
 JAM 276 ... GKKV IYSQPSSTRSEGEFKQTSSFLV...

FIG. 1B

SEQ ID NO:1

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Met Gly Thr Lys Ala Gln Val Glu Arg Lys Lys Leu Leu Cys Lys Phe Ile Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr
1      5      10      15      20      25      30
val His Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val
35      40      45      50      55      60
Glu Trp Lys Phe Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu
65      70      75      80      85      90
Pro Thr Gly Ile Thr Phe Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser Glu Glu Gly Asn Ser Tyr Gly
95      100      105      110      115      120
Glu Val Lys Val Lys Leu Ile Val Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr Ile Gly Asn Arg Ala Val
125      130      135      140      145      150
Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn Pro Lys Ser Thr
155      160      165      170      175      180
Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly Glu Tyr
185      190      195      200      205      210
Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
215      220      225      230      235      240
Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys
245      250      255      260      265      270
Lys Gly Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
275      280      285      290      295      299

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FIG._2

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SEQ ID NO:2
 1 MCILLGLLL GHLTVDTYGR PILEVPESVT GPWKGDVNL P CTYDPLQCYT QVLVKKWLVR GSDPTIFLR DSSGDHIQQA KYQRLHVSH KVPGDVSLQL
 101 STLEMDDRSH YTCEVTWQTP DGNQVRDKI TELRVQKLSV SKPTVTTCSG YGFTVPQGMH ISLQCCARGS PPISYIWKQ QTNQEPKIV ATLSTLLFXP
 ^Glycosaminoglycan attachment site
 201 AVIADSGSYF CTAKQGVSE QHSDIVKFV KDSSKLLKTK TEAPTTMTYP LKATSTVKQS WDWTTDMGY LGETSAGPGK SLPVFAIILI ISLCCMVVFT
 ^Transmembrane domain

FIG._3

301 MAYIMLCRKT SQEHVYEAA R

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OLI2162 (35936.f1)
 SEQ ID NO:12
 TCGCGGAGCTGTGTTCTGTTTCCC
 OLI2163 (35936.p1)
 SEQ ID NO:13
 TGATCGCGATGGGACAAAGGCGCAAGCTCGAGAGGAACTGTTGTGCCT
 OLI2164 (35936.f2)
 SEQ ID NO:14
 ACACCTGGTTCAAAGATGGG
 OLI2165 (35936.r1)
 SEQ ID NO:15
 TAGGAAGAGTTGCTGAAGGCACGG
 OLI2166 (35936.f3)
 SEQ ID NO:16
 TTGCCTTACTCAGGTGCTAC
 OLI2167 (35936.r2)
 SEQ ID NO:17
 ACTCAGCAGTGGTAGGAAAG

FIG._8

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DNA35936 SEQ ID NO:3

CTTCTTGCCA ACTGGTATCA CCTTCAAGTC CGTGACACGG GAAGACACTG 50
GGACATACAC TTGTATGGTC TCTGAGGAAG GCGGCAACAG CTATGGGGAG 100
GTCAAGGTCA AGCTCATCGT GCTTGTGCCT CCATCCAAGC CTACAGTTAA 150
CATCCCCTCC TCTGCCACCA TTGGGAACCG GGCAGTGCTG ACATGCTCAG 200
AACAAGATGG TTCCCCACCT TCTGAATACA CCTGGTTCAA AGATGGGATA 250
GTGATGCCTA CGAATCCCAA AAGCACCCGT GCCTTCAGCA ACTCTTCCTA 300
TGTCTGAAT CCCACAACAG GAGAGCTGGT CTTTGATCCC CTGTCAGCCT 350
CTGATACTGG AGAATACAGC TGTGAGGCAC GGAATGGGTA 390

FIG._4A

consen01 SEQ ID NO:4

TCTCAGTCCC CTCGCTGTAG TCGCGGAGCT GTGTTCTGTT TCCCAGGAGT 50
CCTTCGGCGG CTGTTGTGCT CAGGTGCGCC TGATCGCGAT GGGGACAAAG 100
GCGCAAGCTC GAGAGGAAAC TGTGTGCCT CTTCATATTG GCGATCCTGT 150
TGTGCTCCCT GGCATTGGGC AGTGTTACAG TTGCACTCTT CTGAACCTGA 200
AGTCAGAAAT CCTGAGAATA ATCCTGTGAA GTTGTCTGTG GCCTACTCGG 250
GCTTTTCTTC TCCCCGTGTG GAGTGGAAGT TTGACCAAGG AGACACCACC 300
AGACTCGTTT GCTATAATAA CAAGATCACA GCTTCCTATG AGGACCGGGT 350
GACCTTCTTG CCAACTGGTA TCACCTTCAA GTCCGTGACA CGGGAAGACA 400
CTGGGACATA CACTTGATG GTCTCTGAGG AAGGCGGCAA CAGCTATGGG 450
GAGGTCAAGG TCAAGCTCAT CGTGCTTGTG CCTCCATCCA AGCCTACAGT 500
TAACATCCCC TCCTCTGCCA CCATTGGGAA CCGGGCAGTG CTGACATGCT 550
CAGAACAAGA TGGTTCCCCA CCTTCTGAAT ACACCTGGTT CAAAGATGGG 600
ATAGTGATGC CTACGAATCC CAAAAGCACC CGTGCCTTCA GCAACTCTTC 650
CTATGTCCTG AATCCCACAA CAGGAGAGCT GGTCTTTGAT CCCCTGTCAG 700
CCTCTGATAC TGGAGAATAC AGCTGT 726

FIG._4B

consen02 SEQ ID NO:5

GCAGGCAAAG TACCAGGGCC GCCTGCATGT GAGCCACAAG GTTCCAGGAG 50
ATGTATCCCT CCAATTGAGC ACCCTGGAGA TGGATGACCG GAGCCACTAC 100
ACGTGTGAAG TCACCTGGCA GACTCCTGAT GGCAACCAAG TCGTGAGAGA 150
TAAGATTACT GAGCTCCGTG TCCAGAACT CTCTGTCTCC AAGCCCACAG 200
TGACAACTGG CAGCGGTTAT GGCTTCACGG TGCCCCAGGG AATGAGGATT 250
AGCCTTCAAT GCCAGGGTTC GGGGTTCTCC TCCCATCAGT TATATTTGGT 300
ATAAGCAACA GACTAATAAC CAGGGAACCC ATCAAAGTAG CAACCCTAAG 350
TACCTTACTC TTCAAGCCTG CGGTGATAGC CGACTCAGGC TCCTATTTCT 400
GCACTGCCAA GGGCCAGGTT GGCTCTGAGC AGCACAGCGA CATTGTGAAG 450
TTTGTGGTCA AAGACTCCTC AAAGCTACTC AAGACCAAGA CTGAGGCACC 500
TACAACCATG ACATACCCCT TGAAAGCAAC ATCTACAGTG AAGCAGTCCT 550
GGGACTGGAC CACTGACATG GATGGCTACC TTGGAGAGAC CAGTGCTGGG 600
CCAGGAAAGA GCCTGCCTGT CTTTGCCATC ATCCTCATCA TCTCCTTG TG 650
CTGTATGGTG GTTTTACCA TGGCCTATAT CATGCTCTGT CGGAAGACAT 700
CCCAACAAGA GCATGTCTAC GAAGCAGCCA GGGCACATGC CAGAGAGGCC 750
AACGACTCTG GAGAAACCAT GAGGGTGGCC ATCTTCGCAA GTGGCTGCTC 800
CAGTGATGAG CCAACTTCCC AGAATCTGGG GCAACAATA CTCTGATGAG 850
CCCTGCATAG GACAGGAGTA CCAGATCATC GCCCAGATCA ATGGCAACTA 900
CGCCCGCCTG CTGGACACAG TTCCTCTGGA TTATGAGTTT CTGGCCACTG 950
AGGGCAAAAG TGTCTGTAA AAATGCCCCA TTAGGCCAGG ATCTGCTGAC 1000
ATAATTGCCT AGTCAGTCCT TGCCTTCTGC ATGGCCTTCT TCCCTGCTAC 1050
CTCTCTTCCT GGATAGCCCA AAGTGTCGCG CTACCAACAC TGGAGCCGCT 1100
GGGAGTCACT GGCTTTGCCC TGGGAATTTGC CAGATGCATC TCAAGTAAGC 1150
CAGCTGCTGG ATTTGGCTCT GGGCCCTTCT AGTATCTCTG CCGGGGGCTT 1200
CTGGTACTCC TCTCTAAATA CCAGAGGGAA GATGCCATA GCACTAGGAC 1250
TTGGTCATCA TGCCTACAGA CACTATTCAA CTTTGGCATC TTGCCACCAG 1300
AAGACCCGAG GGGAGGCTCA GCTCTGCCAG CTCAGAGGAC CAGCTATATC 1350
CAGGATCATT TCTCTTTCTT CAGGGCCAGA CAGCTTTTAA TTGAAATTGT 1400
TATTTACAG GCCAGGGTTC AGTTCTGCTC CTCCACTATA AGTCTAATGT 1450
TCTGACTCTC TCCTGGTGCT CAATAAATAT CTAATCATAA CAGCAAAAAA 1500
AAA 1503

FIG. 4C

SEQ ID NO:11 GGAGTCCTT CGCGGGCTGT TGTGTAGTG GCCTGATCGC GATGGGGACA AAGGGCGAAG TCGAGAGGAA ACTGTTGTGC CTCTTCATAT 100
TGGCGATCCT GTTGTGCTCC CTGGCATTGG GCAGTGTTAC AGTGCACCTT TCTGAACCTG AAGTCAGAAT TCCTGAGAAT AATCCTGTGA AGTTGTCCTG 200
TGCTACTCG GGCCTTCTT CTCCCGGTGT GGAGTGGGAG TTGACCAAG GAGACACCAC CAGACTCGTT TGCTATAATA ACAAGATCAC AGCTTCCTAT 300
GAGGACGGG TGACCTTCTT GCCAACTGGT ATCACCTTCA AGTCCGTGAC ACGGGAAGAC ACTGGACAT ACACCTGTAT GGTCTCTGAG GAAGCGGCA 400
ACAGCTATGG GGAGGTCAAG GTCAAGCTCA TCGTGCTTGT GCCTCCATCC AAGCCTACAG TTAACATCCC CTCTCTGCC ACCATTGGGA ACCGGGCAGT 500
GCTGACATGC TCAGAACAAG ATGGTTCCCC ACCTTCTGAA TACACCTGGT TCAAAGATGG GATAGTGATG CCTACGAATC CCAAAAGCAC CCGTGCCTTC 600
AGCAACTCTT CCTATGTCCT GAATCCCACA ACAGGAGAGC TGCTCTTGA TCCCCGTGCA GCCTCTGATA CTGGAGAATA CAGCTGTGAG GCACGGAATG 700
GGTATGGAC ACCCATGACT TCAAATGCTG TCGCATGGA AGCTGTGGAG CGGAATGTGG GGGTCATCGT GGCAGCCGTC CTTGTAACCC TGATTCTCCT 800
GGGAATCTTG GTTTTGGCA TCTGGTTTGC CTATAGCCGA GGCCACTTIG ACAGAACAAA GAAAGGACT TCGAGTAAGA AGGTGATTTA CAGCCAGCCT 900
AGTGCCCGAA GTGAAGGAGA ATTCAACAG ACCTCGTCAT TCCTGGTGTG AGCCTGGTCG GCTCACCSCC TATCATCTGC ATTGSCCTTA CTCAGGTGCT 1000
ACCGGACTCT GGCCCTCTGAT GTCTGTAGTT TCACAGGATG CCTTATTGT CTTCTACACC CCACAGGGCC CCTACTTCT TCGGATGTGT TTTTAATAAT 1100
GTCAGCTATG TGCCCCATCC TCCTTCATGC CCTCCCTCCC TTTCCTACCA CTGCTGAGTG GCCTGGAAT TGTTTAAAGT GTTTATTCCC CATTTCTTTG 1200
AGGATCAGG AAGGAATCCT GGGATGCCA TTGACTTCCC TTCTAAGTAG ACAGCAAAA TGGCGGGGGT TGCACCTCAC TGCCACCTG 1300
GCTGGCAGG ATCTTTGAAT AGGTATCTTG AGCTTGGTTC TGGSCCTCTT CCTTGTGTAC TGACGACCAG GGCCAGCTGT TCTAGAGCGG GAATTAGAGG 1400
CTAGAGCGGC TGAATGGTT GTTTGGTGAT GACACTGGG TCCTTCCATC TCTGGGCCC ACTCTCTTCT GTCTTCCAT GGGAAAGTGCC ACTGGGATCC 1500
CTCTGCCCTG TCCTCCTGAA TACAAGCTGA CTGACATTGA CTGTGCTGT GGAATAATGG AGCTCTTGT GTGGAGAGCA TAGTAAATTT TCAGAGAACT 1600
TGAAGCCAA AGGATTTAAA ACCGCTGCTC TAAAGAAAAG AAACTGGAG GCTGGGCGCA GTGGCTCAG CTGTAATCC CAGAGGCTGA GGCAGCGGA 1700
TCACCTGAG TCGGGAGTTC GGGATCAGCC TGACCAACAT GGAGAAACCC TACTGGAAAT ACAAGTTAG CCAGGCATGG TGGTGCAATG CTGTAGTCCC 1800
AGCTGCTCAG GAGCCTGGCA ACAAGAGCAA AACTCCAGCT CA 1842

FIG.-5

SEQ ID NO:7

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1  CCCACGGCTC GCGCCACGGG TCCGCCGCCA GCGCTCCGGG CCACAGNAG TTTCAGCCTC TTTGGTAGCA GGAGGCTGCA AGAAAGGACA
GGGTGGCGAG GCGGTGGCGC AGGCGGTGCC CCAGCGGGGT GCGCAGGCC CCGTGTCTTC AACTCGGAG AAACCATCGT CCTCCGACCT TCTTCTCTGT

101 GAAGTAGCTC TGGCTGTGAT GGGGATCTTA CTGGGCTGCT TACTCTCTGG GCACCTAACA GTGGACACTT ATGCCCGTCC CATCTCGAA GTGCCAGAGA
CTTCATCGAG ACCGACACTA CCCCTAGAAAT GACCCGGACG ATGAGGACCC CGTGGATTGT CACCTGTGAA TACCGGCAGG GTAGGACCTT CACGGTCTCT

1      SEQ ID NO:2 M G I L L G L L L G L L G H L T V D T Y G R P I L E V P E S
^MET

201 GTGTAACAGG ACCTTGGAAA GGGGATCTGA ATCTTCCCTG CACCTATGAC CCCTGCGCAG GCTACACCCA AGTCTTGGTG AAGTGGCTGG TACAACGTGG
CACATTGTCC TGGAACTTTT CCCCTAGACT TAGAAGGGAC GTGGATACTG GGGACGTTT CCGTGTGGT TCAGAACCAC TTCACCGACC ATGTTGCACC

29  V T G P W K G D V N L P C T Y D P L Q G Y T Q V L V K W L V Q R G

301 CTCAGACCCT GTCACCACTT TTCTACGTGA CTCTTCTGGA GACCATATCC AGCAGGCAAA GTACCAGGGC GCGCTGCATG TCAGCCACAA GGTTCACAGA
GAGTCTGGGA CAGTGGTAGA AAGATGCACT GAGAAACCTT CTGCTATAGG TCCTCCGTTT CATGCTCCCG GCGGACGTAC ACTCGGTGTT CCAAGGTCTT

62  S D P V T I F L R D S S G D H I Q Q A K Y Q G R L H V S H K V P G

401 GATGTATCCC TCCAATTGAG CACCCTGGAG ATGGATGACC GGAGCCACTA CACCTGTGAA GTCACTTGGC AGACTCCTGA TGGCAACCAA GTCGTGAGAG
CTACATAGGG AGGTAACTC GTGGGACCTC TACCTACTGG CCTCGTGTGAT GTGCACACTT CAGTGGACCG TCTGAGGACT ACCGTGCTT CAGCACTCTC

95  D V S L Q L S T L E M D D R S H Y T C E V T W Q T P D G N Q V V R D

501 ATAAGATTAC TGAGCTCCGT GTCCAGAAAC TCTCTGTCTC CAAGCCACA GTGACAACTG GCACCGGTTA TGGCTTCACG GTCCCCCAGG GAATGAGGAT
TATTCTAATG ACTCGAGGCA CAGGTCTTTG AGAGACAGAG GTTCGGGTGT CACTCTTGAC CGTCGCCAAT ACCGAAGTGC CACGGGTGCC CTTACTCCTA

129 K I T E L R V Q K L S V S K P T V T T G S G Y C F T V P Q G M R I

601 TAGCCTTCAA TGCCAGGCTC GGGGTTCTCC TCCCATCAGT TATATTGGT ATAAGCAACA GACTAATAAC CAGCAACCCA TCAAAGTAGC AACCCTAAGT
ATCGGAAGTT ACGGTCCGAG CCCCAGAGG AGGGTAGTCA ATATAAACA TATTCTGTGT CTCATTATTG GTCTTGGT AGTTTCATCG TTGGGATTCA

162 S L Q C Q A R G S P P I S Y I W Y K Q Q T N N Q E P I K V A T L S

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FIG._6A

SEQ ID NO:7 701 ACCTTACTCT TCAAGCCTGC GGTGATAGCC GACTCAGGCT CCTATTCTTG CACTGCCAAG GGCCAGGTTG GCTCTGACCA GCACAGCGAC ATTGTGAAGT
TGGATCAGA AGTTCGGACG CCACTATCGG CTGAGTCCGA GGATAAGAC GTGACGGTTC CCGGTCCAC CGACTCTGT CCGTTCGCTG TAACACTTCA

SEQ ID NO:2 195 T L L F K P A V I A D S G S Y F C T A K G Q V G S E Q H S D I V K F

801 TTGTGGTCAA AGACTCCTCA AAGCTACTCA AGACCAAGAC TGAGGCACCT ACAACCATGA CATACCCTT GAAACAACA TCTACAGTGA AGCAGTCTTG
AACACCAGTT TCTGAGGAGT TTCGATGAGT TCTGGTTCTG ACTCCGTGGA TGTGGTACT GTATGGGAA CTTTCGTTGT AGATGTCAC TCGTCAGGAC

229 V V K D S S K L L K T K T E A P T T M T Y P L K A T S T V K Q S W

901 GGACTGGACC ACTGACATGG ATGGCTACCT TGGAGAGACC AGTGTGGGC CAGGAAGACG CCTGCTGTC TTTCCCATCA TCCTCATCAT CTCCTTGTGC
CCTGACCTGG TGACTGTACC TACCGATGGA ACCTCTCTGG TCACGACCGG GTCTTTCTC GGACGGACAG AACGGTAGT AGGAGTAGTA GAGGAACACG

262 D W T T D H D G Y L G E T S A G P G K S L P V F A I I L I I S L C

1001 TGTATGGTGG TTTTACCAT GGCCTATATC ATGCTCTGTC GGAGACATC CCAACAGAG CATGCTTACG AAGCAGCCAG GTAAGAAAGT CTCTCTCTTT
ACATACCACC AAAAATGGTA CCGGATATAG TACGAGACAG CTTCTGTAG GGTGTTCTC GTACAGATGC TTCTCGGTC CATCTTTCA GAGAGGAGAA

295 C H V V F T M A Y I M L C R K T S Q Q E H V Y E A A R O

1101 CCATTTTGA CCCCCTCCCT CCCCTCAATT TTGATTACTG GCAGGAATG TCGAGGAAG GGGGTGTGGC ACACACCCAA TCCTAAGGCC GGAGCCCTTC
GGTAANAAT GGGCCAGGA CGGAGTTAA AACTAATGAC CGTCTTTAC ACCTCTTCC CCCCACACCG TGCTGGGTT AGGATTCCGG CCTCCGGAAG

1201 AGGTCAGGA CATAGCTGCC TTCCCTCTCT CAGGCACCT CTGAGTTCT TTTGGCCCTC TGAACACAA GGATAATTGA GATCCATCTG CCTTCTGCTT
TCCAGTCTT GTATCGACGG AAGGGAGAGA GTCCGTGGAA GACTCCAA GACTCCAA GACTCCAA ACTTGTTT CTTATTAAAT CTAGGTAGAC GGAAGACGAA

1301 CCAGAAATCCC TGGGTGGTAG GATCCTGATA ATTAATTGCC AAGATTGAG GCAGNAGGTT GGGAAACAG GACCACAGCC CCAAGTCCCT TCTTATGGGT
GGTCTTAGG ACCCACCATC CTAGGACTAT TAATTAACCG TTCTTAATC CGTCTTCCCA CCTTTGGTC CTGGTGTGG GGTTCAGGGA AGAATACCCA

1401 GGTGGGCTCT TGGGCCATAG GGCACATGCC ACAGAGGCCA ACCACTCTGG AGNACCATG AGGGTGGCCA TCTTCCCAAG TGGCTGCTCC AGTATGAGC
CCACCCGAGA ACCCGGTATC CCGTGTACGG TCTCTCCGT TCGTGAGACC TCTTTGGTAC TCCCACCGGT AGAAGGTTT ACCGACGAGG TCACTACTCG

1501 CAACTTCCCA GAATCTGGGC AACAACTACT CTGATGAGCC CTGCATAGGA CAGCAGTACC AGATCATCGC CCAGATCAAT GGCAACTACG CCCGCTGCT
GTTGAAGGTT CTTAGACCCG TTGTTGATGA GACTACTCGG GACGTATCTT GTCTCATGG TCTAGTAGCG GGTCTAGTTA CCGTTGATGC GGGCGGACGA

FIG._6B

SEQ ID NO:7

1601 GGACACAGTT CCTCTGGATT ATGAGTTTCT GGCACACTGAG GGCAAAAGTG TCTGTTAAAA ATGCCCCATT AGCCAGGAT CTGCTGACAT AATTGCCTAG
CCTGTGTCAA GGAGACCTAA TACTCAAGA CCGTGACTC CCGTTTTCAC AGACAATTTT TACGGGGTAA TCCGGTCCTA GACGACTGTA TTAACGGATC

1701 TCAGTCCCTG CCTTCTGCAT GGCTTCTTTC CCTGCTACCT CTCTTCCTGG ATAGCCCCAA GTGTCCGCT ACCAACACTG GAGCCGCTGG GAGTCACTGG
AGTCAGGAAC GGAAGACCTA CCGGAACAAG GGACGATGA GAGAAGGACC TATCGGGTTT CACAGCGGA TGGTTCTGAC CTCGGCGACC CTCAGTGACC

1801 CTTTGGCCCTG GAATTGCGA GATGCATCTC AAGTAAGCCA GCTGCTGGAT TTGGCTCTGG GCCCTTCTAG TATCTCTGCC GGGGGCTTCT GGTACTCCTC
GAAACGGGAC CTTAAACGGT CTACGTAGAG TTCATTCCGT CGACGACCTA AACCGAGACC CGGAAGATC ATAGAGACGG CCCCCGAAGA CCATGAGGAG

1901 TCTAAATACC AGAGGGAAGA TGCCCATAGC ACTAGGACTT GGTCAATCAG CCTACAGACA CTATTCNACT TTGGCATCTT GCCACCAGAA GACCCGAGGG
AGATTTATGG TCTCCCTTCT ACGGTATCG TGATCTGMA CCAGTAGTAC GGATGCTGT GATAAGTTGA AACCGTAGAA CCGTGGTCTT CTGGGCTCCC

2001 AGGCTCAGCT CTGCCAGCTC AGAGGACCAG CTATATCCAG GATCATTTCT CTTTCTTTCAG GCCCAGACAG CTTTAAATG AATGTGTAT TTCACAGGCC
TCCGAGTCCA GACGGTCGAG TCTCCTGTC GATATAGGTC CTAGTAAAGA GAAAGMAGTC CCGTCTCTC GMAATTAAC TTTAACAAATA AAGTGTCCGG

2101 AGGGTTCACT TCTGCTCCTC CACTATAAGT CTATGTCTT GACTCTCTCC TGGTCTCMA TAAATATCTA ATCATACAG C
TCCCAAGTCA AGACGAGGAG GTGATATTCA GATTACAGA CTGACAGAGG ACCACGAGTT ATTTATAGAT TAGTATTGTC G

FIG..6C

SEQ ID NO:8

CCCAGAAGTTCAAGGGCCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCTCGACCTCCT
CAGAGCAGCCGGCTGCCGCCCGGGAAGATGGCGAGCAGGAGCCGCCACCGCCTCCTCCT
GCTGCTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTTCTGC
CCCAAAGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAA
AACCCCAAGAAGACTGTTTCCTCCAGATTAGAGTGGAAGAACTGGGTTCGGAGTGTCTC
CTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGA
TTTCAATATCCGGATCAAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGT
TAGTGCCCCATCTGAGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATT
AGTGGCTCCAGCAGTTCCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGAAGTGTGGT
AGAGCTACGATGTCAAGACAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTAAGGA
TGGCATCCGTTTGCTAGAAAATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATACAC
AATGAATACAAAACTGGAAGTCTGCAATTTAATACTGTTTCCAACTGGACACTGGAGA
ATATTCCTGTGAAGCCCGCAATTCTGTTGGATATCGCAGGTGTCCTGGGAAACGAATGCA
AGTAGATGATCTCAACATAAGTGGCATCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGAT
TTCCGTTTGTGGCCTTGGTGTATGCTATGCTCAGAGGAAAGGCTACTTTTCAAAGAAAC
CTCCTTCCAGAAGAGTAATTCTTCATCTAAAGCCACGACAATGAGTGAAAATGTGCAGTG
GCTCACGCCTGTAATCCCAGCACTTTGGAAGGCCGCGGCGGGCGGATCACGAGGTCAGGA
GTTCTAGACCAGTCTGGCCAATATGGTGAAACCCCATCTCTACTAAAATACAAAATTAG
CTGGGCATGGTGGCATGTGCCTGCAGTTCAGCTGCTTGGGAGACAGGAGAATCACTTGA
ACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGCCACTGCAGTCCAGCCTGGGTAA
CAGAGCAAGATTCCATCTCAAAAAATAAAATAAATAAATAAATAAATAAATACTGGTTTTTACC
TGTAGAATTCTTACAATAAATATAGCTTGATATTC

FIG._7

SEQ ID NO:9

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSR
LEWKKLGRSVSFVYYQOTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN
LEEDTVTLEVLVAPAVPSCVPPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR
LGSQSTNSSYTMNTKTGTTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGI
IAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALW
KAAAGGSRGQEF

FIG._11

SEQ ID NO:5

1 GCAGGCAAG TACCAGGGCC GCCTGCATGT GACCCACMAG GTTCCAGGAG ATGTATCCCT CCAATTGACC ACCCTGGAGA TGCATGACCG GAGCCACTAC
 CGTCCGTTTC ATGCTCCCG CGGACGTACA CTCGGTGTTT CMAAGTCCTC TACATAGGGA GGTAACTCG TGGGACCTCT ACCTACTGGC CTCGGTGATG
 ^42257.f1 SEQ ID NO:18 ^42257.p1 SEQ ID NO:22

101 ACGTGTGAG TCACCTGGCA GACTCCTGAT GGCACCAAG TCGTGAGAGA TAAGATTACT GAGCTCCGTG TCCAGAACT CTCTGTCTCC AAGCCACAG
TGCACACTTC AGTGGACCGT CTGAGGACTA CCGTGGTTC ACCACTCTCT ATTCTAATGA CTCGAGGCAC AGGTCTTTGA GACACAGAGG TTCGGGTGTC

201 TGACAACTGG CAGCGGTTAT GGCTTCACGG TGCCCCAGGG AATGAGGATT AGCCTTCAAT GCCAGGGTTC GGGGTCTCTCC TCCCATCAGT TATATTGCT
 ACTGTTGACC GTCGCCAATA CCGAAGTGCC ACGGGGTCCC TTACTCCTAA TCGGACGTTA CGGTCCCAAG CCCCAGAGG AGGTAGTCA ATATAAACCA

301 ATAAGCAACA GACTAATAAC CAGGGAACCC ATCAAGTAG CAACCTAAG TACCTTACTC TTCMAGCCTG CCGTGATAGC CGACTCAGGC TCCTATTCT
 TATTGCTGT CTGATTATTG GTCCCTTGGG TACTTTTCATC GTTGGGATTG ATGGAATGAG AAGTTCGGAC GCCACTATCG GCTGAGTCCG AGGATAAAGA

401 GCACTGCCAA GGGCCAGGTT GGCTCTGAGC AGCAGAGCGA CATTGTGAAG TTTGTGGTCA AAGACTCCTC AAAGCTACTC AAGACCAAGA CTGAGGCACC
CGTGACGGTT CCCGGTCCAA CCGAGACTCG TCGTGTGCTGCT GTAACACTTC AAMACCCAGT TTCTGAGGAG TTTCGATGAG TTCTGGTTCT GACTCCGTGG
 ^42257.f1 SEQ ID NO:20

501 TACAACCATG ACATACCCCT TGAAGCAAC ATCTACAGTG AAGCAGTCCT GGGACTGGAC CACTGACATG GATGGCTACC TTGGAGAGAC CACTGCTGGG
 ATGTTGGTAC TGTATGGGA ACTTTCGTTG TAGATGTCAC TTGCTCAGGA CCTTGACCTG GTGACTGTAC CTACCCGATGG AACCTCTCTG GTCACGACCC

601 CCAGGAAGA GCCTGCCCTGT CTTTGCCATC ATCCTCATCA TCTCCTTGTG CTGTATGGTG GTTTTACCCTA TGGCCTATAT CATGCTCTCT CGGAAGACAT
 GGTCTTTCT CGGACGGACA GAAACGGTAG TAGGACTAGT AGAGGACAC GACATACCAC CAAAATGGT ACCGGATATA GTACGAGACA GCCTTCTGTA
 ^42257.f2 SEQ ID NO:19

701 CCCAACAAGA GCATGTCTAC GAAGCAGCCA GGGACATGCG CAGAGAGGCC AAGCACTCTG GAGAACCAT GAGGGTGCC ATCTTCGCAA GTGGCTGCTC
 GGGTGTCTT COTACAGATG CTTCTGCGGT CCCGTCTACG GTCTCTCCGG TTGCTGAGAC CTCTTTGGTA CTCCCACCGG TAGAAGCGTT CACCGACGAG

FIG._9A

SEQ ID NO:5

801 CAGTGATGAG CCAACTTCCC AGAATCTGGG GCACAACATA CTCTGATGAG CCTGTCATAG GACAGGAGTA CCAGATCATC GCCCAGATCA ATGGCAACTA
GTCACTACTC GGTGGAAGG TCTTAGACCC CGTTGTTGAT GAGACTACTC GGGACGTATC CTGTCTCAT GGTCTAGTAG CCGGTCTAGT TACCCTTGAT

901 CGCCCGCCCTG CTGGACACAG TTCCTCTGGA TTATGAGTTT CTGGCCACTG AGGGCAAAAG TGCTCTTTAA AAATGCCCCA TTAGGCCAGG ATCTGCTGAC
CGGGCGGAC GACCTGTGTC AAGGAGACCT AATACTCAAA GACCGGTGAC TCCCGTTTTT ACAGACAATT TTACGGGGT ATCCGGTCC TAGACGACTG

1001 ATAATTGCCT AGTCAGTCCT TGCCTTCTGC ATGGCCTTCT TCCCTGCTAC CTCTCTTCCT GGATAGCCCCA AAGTGTCCGC CTACCAACAC TGGAGCGGCT
TATTAACGA TCAGTCAGGA ACGBAAGACG TACCGGAAGA AGGGACGATG GAGAGAAGGA CCTATCGGT TTCACAGGCG GATGGTTGTG ACCTCGGCGA

1101 GGGAGTCACT GGCTTTGCCC TGGAAATTGC CAGATGCATC TCAAGTAAGC CAGCTGCTGG ATTTGGCTCT GGGCCCTTCT AGTATCTCTG CCGGGGGCTT
CCCTCAGTGA CCGAAACGGG ACCTTAAACG GTCTACGTAG AGTTCATTCTG GTGAGCAGACC TAAACCGAGA CCGGGGAAGA TCATAGAGAC GGGCCCCGAA

1201 CTGTACTCC TCCTAAATA CCAGAGGGAA GATGCCCATTA GCACTAGGAC TTGGTCAATCA TGCCTACAGA CACTATTCAA CTTTGGCATC TTGCCACCAG
GACCATGAGG AGAGATTTAT GGTCTCCCTT CTACGGGTAT CGTGATCCTG AACCAGTAGT ACGGATGTCT GTGATAAGTT GAAACCGTAG AACGGTGGTC

1301 AAGACCCGAG GGGAGGCTCA GCTCTGCCAG CTCAGAGGAC CAGCTATATC CAGGATCATT TCTCTTTCTT CAGGGCCAGA CAGCTTTTAA TTGAAATTCT
TTCTGGGCTC CCTCCGAGT CGAGACGGTC GAGTCTCCTG GTCGATATAG GTCCTACTAA AGAGAAAGAA GTCCGGGTCT GTCGAAAATT AACTTTAACA

1401 TATTTACAG GCCAGGGTTC AGTTCTGCTC CTCCTACTATA AGTCTAATGT TCTGACTCTC TCCTGTGTCT CAATAAATAT CTAATCATAA CAGCAAAAAA
ATAAGTGTG CGGTCCCAAG TCAAGACGAG GAGGTGATAT TCAGATTACA AGACTGAGAG AGGACCACGA GTTATTATTA GATTAGTATT GTCGTTTTTT

^42257.r2 SEQ ID NO:21

1501 AAA

TTT

FIG._9B

PCT 30

A33 HUMAN - A33 ANTIGEN PRECURSOR - HOMO SAPIENS (319 aa)

SCORE = 246 (86.6 BITS), EXPECT = 2.8e-19, P = 2.8e-19

IDENTITIES = 81/268 (30%), POSITIVES = 131/268 (48%), AT 121,17, FRAME = +1

DNA40628 121 LALGSVTVHSSEPEVRIPENNPVKLSAYSGFSSPR--VEW-KFDQGDTRLVC--YNN

SEQ ID NO:23

DNA40628 283 K--ITAS-YEDRVTF-----PTGTFKSVTREDTGTYTCMV-----EEGNSYGEVKVK

A33 human 77 KNYIHGELYKNRVVISNNAEQSDASITIDQLTMADNGTYECSVSLMSDLEGNT--KSRVR

DNA40628 427 LIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGPPSEYTWFKDGI VMP TNP KSTRAFSN

A33 human 135 LLVLVPPSKPECGIEGETIIGNNIQLTCQSKEGSPTPQYSWKRYNILLNQEQP-----

DNA40628 607 SSYVLNPTTGELV-FDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVG--IVA

A33 human 187 ---LAOPASGQPVSLKNISTDTSGYYICTSSNEEGTQFCNITTVAVRSPSMNVALYVGIAY

DNA40628 775 AVLVTLLILGILVFGIWFAYSRGHFDRT--KKGTSKKVIYSQP

[illegible]

EIC 10A

SCORE = 245 (86.2 BITS), EXPECT = 3.6e-19, P = 3.6e-19

DNA40628 112 LC SL--ALGSVTVHSSEPEVRIPENNPVKLS CAYSGFSSPR---VEW-KFDQGD TTRLVC
 SEQ ID NO:25
 *** * . . * . * * * . * * . * * * * *
 A33 human 12 LCAVRTVDAISVETPQDVLRASQKGKSVTL PCTYHTSTSSREGLIQWDKLLLTHTERVVI
 SEQ ID NO:26

DNA40628 274 --YNNK--ITAS-YEDRVTFLL-----PTGITFKSVTREDTGTYTCTMVSSEEGGNSYGEVK

 113 human 72 WPFSSKNVYIHGELYKNRVVISNNAEQSDASITIDQLTMADNGTYECSVSLMS-DLEGNTK

DNA40628 421 --VKLIVLPSPKPTVNIPSSATIGNRAVLTCEQDGPSEYTFWKDGIWPTNPKSTR
 ..***** * *** *** ..*** .*. *
 131 SRVRLIVLPSPKPEGIEGETIIGNNIQLTCOSKEGSTTPQYSWKRYNILNQEQP----

DNA40628 595 AFSNSSYVLNPTTGELV - FDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGV --
 187 -----IAOPASGOPVSIKNISTDTSGYYICTSSNEEGTOFCNITVAVRSPSMVALYV

DNA40628 766 -I V A A V L V T L I L G I L V F G I W F A Y S R G H F D R T -- K K G T S S K K V I Y S Q P
 * * . * * . * * . * * . * * . * * . * * . * * . * * . * * . * * . * * . * * . * * . *
 A23 human 240 G I A V G V A A L I I G I I I Y -- C C C C R G K D N T E D K E D A R P N R E A Y E E P

FIG. 10B

FIG. 12

FIG. 12

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SEQID NO: 6  A33_hum  1  M V G K M W P V L W T L C A V R V T V D A I S V E T P Q D V L R A S Q G K S V T L P C T Y H T S T S
SEQID NO: 2  45416  1  - M G I L L G L L L L G H L T V D T Y G R P I L E V P E S V T G P W K G - D V N L P C T Y D P L O G

A33_hum      51  S R E G L I Q W D K L L L T H T E R V V I I W - P F S N K N Y I I H G E L Y K N R V S I S N N A E Q S D
45416        49  Y T Q V L V K W - - L V Q R G S D P V T I I F L R D S S G D H I Q Q A K Y Q G R L H V S H K V - P G D

A33_hum     100  A S I T I D Q L T M A D N G T Y E C S V S - L M S D L E G N T K S R V - - - - - R L L V L V P P S
45416        96  V S L Q L S T L E M D O R S H Y T C E V T W O T P D G N Q V V R D K I T E L R V Q K L S V S K P T V

A33_hum     143  K P E C G I E G E T I I G N N I Q L T C Q S K E G S P T P Q Y S W K R Y N I L N Q E Q P L A Q P A S
45416       146  T T G S G Y G F T V P Q G M R I S L Q C Q A R - G S P I S Y I W - - Y K Q Q T N N Q E P I K V A T

A33_hum     193  G Q P V S L K N I S T D T S G Y Y I C T S S N E E G T - Q F C N I - T V A V R S P S M N V A L Y V G
45416       193  L S T L L F K P A V I A D S G S Y F C T A K G Q V G S E Q H S D I I V K F V V K D S S K L L K T K T E

A33_hum     241  I A V G V V A A L I I I G I I I Y C C C C R G K D D N T E D K E D A R P N R E A Y E E P P E Q L R E
45416       243  A P T T M T Y P L K A T S T V K S W D W T T D M D G Y L G E T S A G P G X S L P V F A I I L I I S

A33_hum     291  L S R E R E E E D D Y R Q E E Q R S T G R E S P D H L D Q
45416       293  L C C H V V F T M A Y I M L C R K T S Q Q E H V Y E A A R

```

FIG.-13

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|---|----|--------|----|---|---|---|---|---|---|---|---|---|---|---|----|----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | .. | HVGKMW | PV | W | T | L | C | A | V | R | V | T | V | D | .. | .. | A | I | S | V | E | T | P | O | D | V | L | R | A | S | Q | G | K | S | V | T | L | P | C | | | | | | | | | |
| 1 | M | A | R | R | S | R | H | R | L | L | L | L | R | Y | L | V | V | A | L | G | Y | H | K | A | Y | G | F | S | A | P | K | D | Q | Q | V | V | T | A | V | E | Y | Q | E | A | I | L | A | C |

1 MARRSRHRLLLRLRYLVVALGYHKA YGFSAPKDDQQVVVTAVVEYQEA ILLAC

44 TYHT STSSREG L I Q W D K L L L T H T E R V V I W P F S N K N Y I H G E L Y K N R V S I S N
51 . . X T P K K T V S S R L E W K K L G R S V S F V Y Y Q Q T . L O G D . F K N R

51 . . K T P K K T V S S R L E W K X L G A S V S F V Y Y Q O T . L Q G D . F K N R

94 N A E Q S O A S I T I D Q L T W A D N G T Y E C S V S L M S D L E G N . T K S R V R L L V L V P P S
87 . A E M I D F N I R I K N V T R S D A G K Y Y R C E V S A P S E Q G Q N L E E D T V T L E E V L V A P A

87 - A E M I D F N I R I K N V T R S D A G K Y R C E V S A P S E Q G O N L E E D I V I L E V L V A P A

143. X P E C G I E G E T I I G N H I O L T C O S K E G S P T P Q Y S W K R Y N I L N O E Q P L A O P A S

136 V P S C E V P S S A L S G T V V E L R C O D K E G N P A P E Y T W F K D G I R L L E N P R L G S O S

136 V P S C E V P S S A L S G T V V E L R C Q D K E G N P A P E Y T W F K D G I R L L E N P R L G S O S

193 G Q P V S L K N I S T D T S G Y Y I C T S S N E E G T O F C N I T V A V . . . R S P S M N V A L Y V
186 T N S S Y T M N T X T G T L O F N T . V S K L D T G E Y S C E A R N S V G Y R R C P G K R M O V D D

186 T N S S Y T M N T X T G T L O F N T . V S K L D T G E Y S C E A R N S V G Y R R C P G K R M Q V D D

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 240 | G | I | A | V | G | V | V | A | L | I | I | G | I | I | Y | C | C | R | G | X | D | D | N | T | E | O | K | E | D | A | R | P | N | R | E | A | Y | E | E | P | E | | | | | | |
| 235 | L | N | I | S | G | I | I | A | V | V | V | V | A | L | V | I | S | V | C | G | L | G | V | C | Y | A | O | R | K | G | Y | F | S | K | E | T | S | F | O | K | S | N | S | S | K | A | T |

235 L N I S G I I A A V V V V A L V I I S V C G L G V C Y A Q R K G Y F S K E T S F Q K S H S S S K A T T

287 QLRELSR.EREEEDDYRQEEQRS TGRSPDHLDO
285 MSENVQWLT PVI PAL WKAAAGGS RGOEF

285 M S E N V Q W L T P V I P A L W X A A A G G S R G Q E F

SEQ ID NO: 10 jam 1 MGT E G K A G R K L L F L F T - S M I L G S L V Q G K G S V Y T A Q S D V Q V P E N E S I K L T C
 SEQ ID NO: 1 40628 1 MGT K A O V E R K L L C L F I L A I L L C S L A L G S V T V H S S E P E V R I P E N N P V K L S C

jam 50 T Y S G F S S P R V E W K F V Q G S T T A L V C Y N S Q I T A P Y A D R V T F S S S G I T F S S V T
 40628 51 A Y S G F S S P R V E W K F D Q G D T T R L V C Y N N K I T A S Y E D R V T F L P T G I T F K S V T

jam 100 R K D N G E Y T C M V S E E G G Q N Y G E V S I H L T V L V P P S K P T I S V P S S V T I G N R A V
 40628 101 R E D T G T Y T C M V S E E G G N S Y G E V K V K L I V L V P P S K P T V N I P S S A T I G N R A V

jam 150 L T C S E H D G S P P S E Y S W F K D G I S M L T A D A K K T R A F M N S S F T I D P K S G D L I F
 40628 151 L T C S E Q D G S P P S E Y T W F K D G I . V M P T N P K S T R A F S N S S Y V L N P T T G E L V F

jam 200 D P V T A F D S G E Y Y C Q A Q N G Y G T A M R S E A A H M D A V E L N V G G I V A A V L V T L I L
 40628 200 D P L S A S D T G E Y S C E A R N G Y G T P W T S N A V R M E A V E R N V G V I V A A V L V T L I L

jam 250 L G L L I F G V W F A Y S R G Y F E T T K K G T A P G K K V I Y S Q P S T R S E G E F K Q T S S F L
 40628 250 L G I L V F G I W F A Y S R G H F D R T K K G T . S S K K V I Y S Q P S A R S E G E F K Q T S S F L

jam 300 V
 40628 299 V

FIG. 15

SEQ ID NO: 10 jam 1 M G T E G K A G R K L L F L F T S M I L G S L V Q G K G S V Y T A Q S D V Q V P E N E S I K L T
 SEQ ID NO: 2 45416 1 M G I L L G L L L G H L T V D T Y G R P I L E V P E S V T G P W K G D V N L P

49 C T Y S . . . G F S S P R V E W K F V Q G S T T A L V . . . C Y N S Q I T A P Y A D R V T F S .
 45416 41 C T Y D P L Q G Y T Q V L V K W L V Q R G S O P V T I F L R D S S G D H I Q Q A K Y Q G R L H V S H

90 S S G I T F S S V T R K D N G E Y T C M V . . . S E E G G Q N Y G E V S I H L T V L V P P
 45416 91 K V P G D V S L Q L S T L E M D O R S H Y T C E V T W O T P D G N Q V V R D K I T E L R V Q K L S V

132 S K P T I S V P S S V T I G N R A V L T C S E H D G S P P S E Y S W F K D G I S M L T A D A
 45416 141 S K P T V T T G S G Y G F T V P Q G M R I S L Q C Q A R G S P P I S Y I W Y K Q O T N . . N Q E P

178 K K T R A F M N S S F T I D P K S G D L I F D P V T A F D S G E Y Y C Q A Q N G Y G T A M R S E A A
 45416 188 I K V A T L S T L L F K P A V I A D S G S Y F C T A K G O V G S E Q H S D I V

228 H . . . M D A V E L N V G G I V A A V L V T L I L L G L L I F G . . . V W F A Y S R G Y F E T T K K
 45416 227 K F V V K D S S K L L K T K T E A P T T M T Y P L K A T S T V K Q S W D W T T D M D G Y L G E T S A

jam 272 G T A P G K K V I Y S O P S T R S E G E F K Q T S S F L V
 45416 277 G P G K S L P V F A I I L I S L C C M V V F T M A Y I M L C R K T S Q Q E H V Y E A A R

FIG. 16

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SEQ ID NO: 10 jam 1 M G T E G K A G R K L L F L F T S M I L G S L V Q G K G S V Y T A Q S D V Q V . . . P E N E S I K L
SEQ ID NO: 29 35638 1 . . W A R R S R H R L L L L R Y L V V A L G Y H K A Y G F S A P K Q Q V T A V E Y Q E A I L

jam 48 T C . T Y S G F S S P R V E W K F V Q G S T T A L V C Y N S Q I T A P Y A D R V T F S S G I T F S
35638 49 A C K T P K X T V S S R L E W K K L . G R S V S F V Y Y Q Q T L Q G D F K N R A E M I D F N I R I K

jam 97 S V T R K D N G E Y T C M V S . . E E G G Q N Y G E V S I H L T V L V P P S K P T I S V P S S V T I
35638 98 N V T R S D A G K Y R C E V S A P S E Q G Q N L E E D T V T L E V L V A P A V P S C E V P S S A L S

jam 145 G N R A V L T C S E H D G S P P S E Y S W F K D G I S M L T A D A K K T R A F M N S S F T I D P K S
35638 148 G T V V E L R C O D K E G N P A P E Y T W F K D G I R L L . E N P R L G S Q S T N S S Y T M N T K T

jam 195 G D L I F D P V T A F D S G E Y Y C Q A Q N G Y G T A H R S E A A H M D A V E L N V G G I V A A V L
35638 197 G T L Q F N T V S K L D T G E Y S C E A R N S V G . Y R R C P G K R M Q V D D L N I S G I I A A V V

jam 245 V T L I L L G L L I F G V W F A Y S R G Y F E T T K K G T A P G K K V I Y S Q P S T R S E G E F K Q
35638 246 V V A L V I S V C G L G V C Y A Q R K G Y F . . . S K E T S F O K S N S S S K A T T M S E N V Q W L

jam 295 T S S F L V
35638 293 T P V I P A L W K A A A G G S R G Q E F

FIG._17

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SEQ ID NO: 6 A33_hum 1 M V G K M W P V L W T . L C A V R V T V D A I S V E T P Q D V L R A S Q G K S V T L P C T
 SEQ ID NO: 10 jam 1 M G T E G K A G R K L L F L F T S M I L G S L V O G K G S V Y T A Q S D V O V P E N E S I K L T C T

A33_hum 45 Y H T S T S S R E G L I Q W D K L L L T H T E R V V I W P F S N K N Y I I H G E L Y K N R V S I S N N
 jam 51 Y S G F S S P R . . . V E W . K F V O G S T T A L V C . . Y N S Q . . I T A P . Y A D R V T F S S .

A33_hum 95 A E Q S D A S I T I D Q L T M A D N G T Y E C S V S L M S D L E G N T K S R V R L L V L V P P S K P
 jam 91 S G I T F S S V T R K D N G E Y T C M V S E E G G . Q N Y G E V S I H L T V L V P P S K P

A33_hum 145 E C G I E G E T I I G N N I O L T C Q S K E G S P T P O Y S W K R Y N I L N Q E Q P L A Q P A S G Q
 jam 135 T I S V P S S V T I G N R A V L T C S E H D G S P S E Y S W F K D G I S M L T A D A K K T R A F M

A33_hum 195 P V S L K N I S T D T S G Y Y I C T S S N E E G T O F C N I T V A V R S P S M N . . . V A L
 jam 185 N S S F T I D P K S G D L I F D P V T A F D S G E Y Y C Q A Q N G Y G T A M R S E A A H M D A V E L

A33_hum 238 Y V . G I A V G V V A A L I I G I I I Y C . . . C C C R G K D D N T E D K E D A R P N R E A Y E E
 jam 235 N V G G I V A A V L V T L I L L G L L I F G V W F A Y S R G Y F E . T T K K G T A P G K K V I Y S Q

A33_hum 284 P P E O L R E L S R E R E E E D D Y R Q E E Q R S T G R E S P O H L D Q
 jam 284 P S T R S E G E F K Q T S S F L V

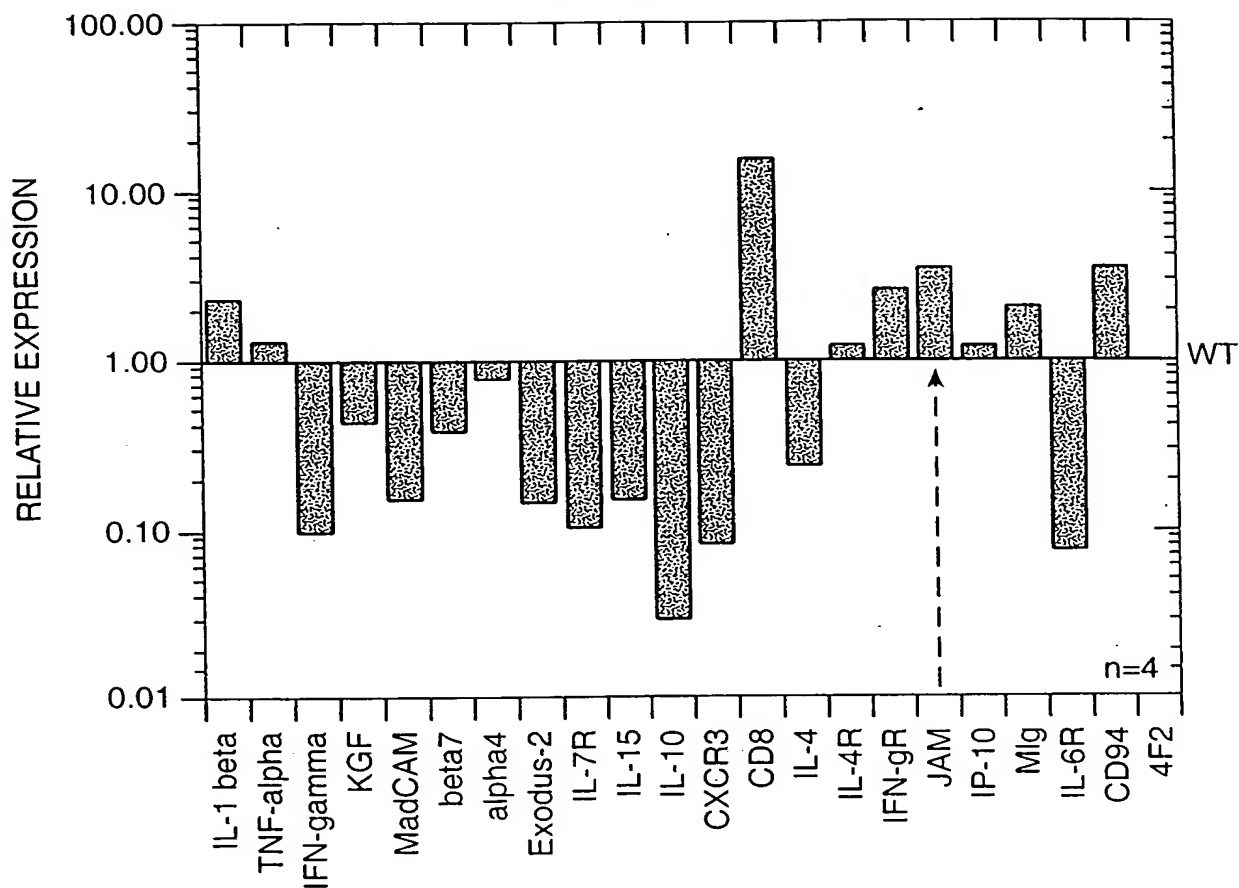
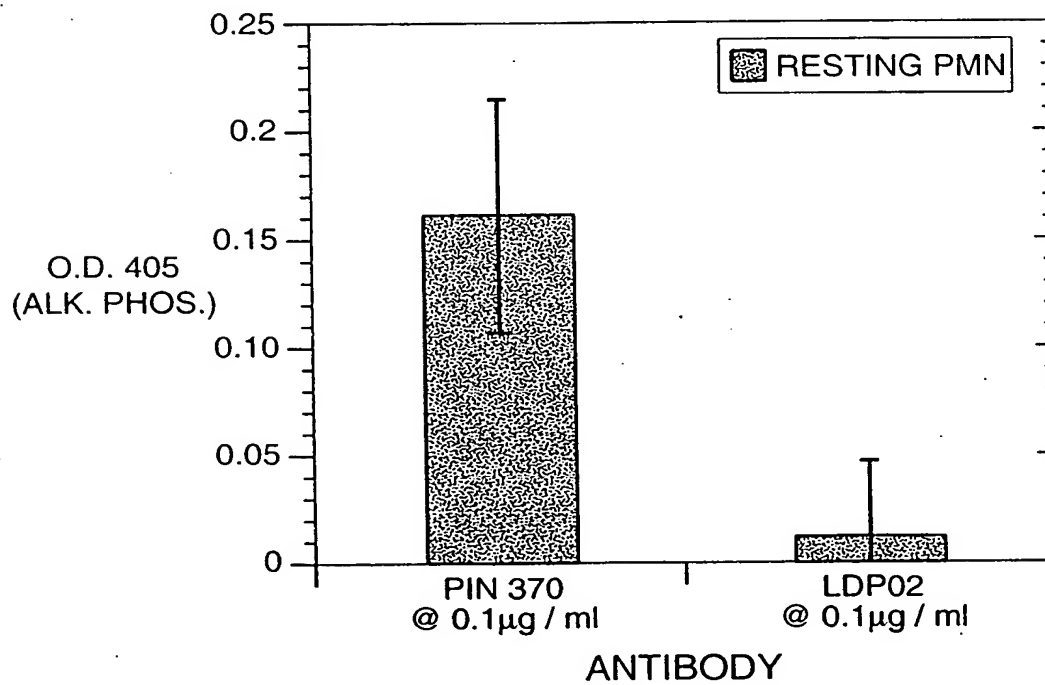
FIG.-18

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| <u>TISSUE</u> | <u>EXPRESSION</u> | <u>TISSUE</u> | <u>EXPRESSION</u> | <u>TISSUE</u> | <u>EXPRESSION</u> |
|-------------------|-------------------|-----------------|-------------------|----------------------|-------------------|
| WHOLE BRAIN | + | HEART | ++ | KIDNEY | +++ |
| AMYGDALA | + | AORTA | + | LIVER | ++ |
| CAUDATE NUCLEUS | + | SKELETAL MUSCLE | + | SMALL INTESTINE | ++ |
| CEREBELLUM | - | COLON | +++ | SPLEEN | ++ |
| CEREBRAL CORTEX | + | BLADDER | ++ | THYMUS | ++ |
| FRONTAL LOBE | + | UTERUS | + | PERIPHERAL LEUKOCYTE | + |
| HIPPOCAMPUS | + | PROSTATE | +++ | LYMPH NODE | + |
| MEDULLA OBLONGATA | + | STOMACH | +++ | BONE MARROW | + |
| OCCIPITAL LOBE | + | TESTIS | ++ | | |
| PUTAMEN | + | OVARY | +++ | APPENDIX | + |
| SUSTANTIA NIGRA | + | PANCREAS | ++ | LUNG | ++++ |
| TEMPORAL LOBE | + | PITUITARY GLAND | ++ | TRACHEA | ++++ |
| THALAMUS | + | ADRENAL GLAND | ++ | PLACENTA | ++++ |
| NUCLEUS ACCUMBEUS | + | THYROID GLAND | ++ | | |
| SPINAL CORD | - | SALIVARY GLAND | +++ | FETAL BRAIN | + |
| | | MAMMARY GLAND | ++ | FETAL HEART | + |
| | | | | FETAL KIDNEY | ++ |
| | | | | FETAL LIVER | +++ |
| | | | | FETAL SPLEEN | + |
| | | | | FETAL LUNG | ++++ |

FIG._19

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**FIG. 20****FIG. 21**